

1600#21

CRF Errors Corrected by the STIC Systems Branch

CRF Processing Date: 2/24/2003

Edited by: [Signature]

Verified by: [Signature] (STIC staff)

Serial Number: 09/771,904A

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically:

- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included:

- ☐ Deleted extra, invalid, headings used by an applicant, specifically:

- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically:

- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically:

- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seq 64 - aligned amino acid nos.

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.



RAW SEQUENCE LISTING

DATE: 02/24/2003

PATENT APPLICATION: US/09/771,904A

TIME: 12:18:15

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\02242003\I771904A.raw

```

4 <110> APPLICANT: DeBonte, Lorin R.
5       Fan, Zhegong
6       Miao, Guo-Hua
8 <120> TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
10 <130> FILE REFERENCE: 07148-063003
12 <140> CURRENT APPLICATION NUMBER: US 09/771,904A
13 <141> CURRENT FILING DATE: 2001-01-29
15 <150> PRIOR APPLICATION NUMBER: US 08/874,109
16 <151> PRIOR FILING DATE: 1997-06-12
18 <160> NUMBER OF SEQ ID NOS: 70
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1155
24 <212> TYPE: DNA
25 <213> ORGANISM: Brassica napus
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)...(1152)
30 <223> OTHER INFORMATION: Wild type Fad2
32 <221> NAME/KEY: misc_feature
33 <222> LOCATION: 205
34 <223> OTHER INFORMATION: n = a, g, c, or t/u
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37 atg ggt gca ggt gga aga atg caa gtg tct cct ccc tcc aag aag tct      48
38 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
39   1           5           10           15
41 gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act      96
42 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
43           20           25           30
45 gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg      144
46 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
47           35           40           45
49 atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc      192
50 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ala Ser
51   50           55           60
W--> 53 tgc ttc tac tac ntc gcc acc act tac ttc cct ctc ctc cct cac cct      240
54 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
55   65           70           75           80
57 ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc      288
58 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
59           85           90           95
61 cta acc ggc gtc tgg gtc ata gcc cac gaa tgc ggc cac cac gcc ttc      336
62 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe

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63	100	105	110	
65	agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc	384		
66	Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser			
67	115 120 125			
69	ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cgc agc cac	432		
70	Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His			
71	130 135 140			
73	cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag	480		
74	His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys			
75	145 150 155 160			
77	aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg	528		
78	Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu			
79	165 170 175			
81	gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg ccg ttg	576		
82	Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu			
83	180 185 190			
85	tac tta gcc ttc aac gtc tcg gga aga cct tac gac ggc ggc ttc cgt	624		
86	Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg			
87	195 200 205			
89	tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc	672		
90	Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu			
91	210 215 220			
93	cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc	720		
94	Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu			
95	225 230 235 240			
97	ttc cgt tac gcc gcc ggc cag gga gtg gcc tcg atg gtc tgc ttc tac	768		
98	Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr			
99	245 250 255			
101	gga gtc ccg ctt ctg att gtc aat ggt ttc ctc gtg ttg atc act tac	816		
102	Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr			
103	260 265 270			
105	ttg cag cac acg cat cct tcc ctg cct cac tac gat tcg tcc gag tgg	864		
106	Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp			
107	275 280 285			
110	gat tgg ttc agg gga gct ttg gct acc gtt gac aga gac tac gga atc	912		
111	Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile			
112	290 295 300			
114	ttg aac aag gtc ttc cac aat att acc gac acg cac gtg gcc cat cat	960		
115	Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His			
116	305 310 315 320			
118	ccg ttc tcc acg atg ccg cat tat cac gcg atg gaa gct acc aag gcg	1008		
119	Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala			
120	325 330 335			
122	ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg	1056		
123	Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val			
124	340 345 350			
126	gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg	1104		
127	Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro			
128	355 360 365			

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130 gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta      1152
131 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
132   370                               375                               380
134 tga                                                                    1155
136 <210> SEQ ID NO: 2
137 <211> LENGTH: 384
138 <212> TYPE: PRT
139 <213> ORGANISM: Brassica napus
141 <220> FEATURE:
142 <223> OTHER INFORMATION: Xaa = Phe, Leu, Ile, or Val
144 <400> SEQUENCE: 2
145 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
146   1      5      10      15
147 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
148      20      25      30
149 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
150      35      40      45
151 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
152      50      55      60
W--> 153 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
154   65      70      75      80
155 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
156      85      90      95
157 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
158      100     105     110
159 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
160      115     120     125
161 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
162      130     135     140
164 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
165 145      150     155     160
166 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
167      165     170     175
168 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
169      180     185     190
170 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
171      195     200     205
172 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
173      210     215     220
174 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
175 225      230     235     240
176 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
177      245     250     255
178 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
179      260     265     270
180 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
181      275     280     285
182 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
183      290     295     300

```

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DATE: 02/24/2003

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TIME: 12:18:15

Input Set : A:\PTO.AMC.txt

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184 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 185 305 310 315 320
 186 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
 187 325 330 335
 188 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
 189 340 345 350
 190 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
 191 355 360 365
 192 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 193 370 375 380

195 <210> SEQ ID NO: 3

196 <211> LENGTH: 1155

197 <212> TYPE: DNA

198 <213> ORGANISM: Brassica napus

200 <220> FEATURE:

201 <221> NAME/KEY: CDS

202 <222> LOCATION: (1)...(1152)

203 <223> OTHER INFORMATION: G to A transversion mutation at nucleotide 316

205 <221> NAME/KEY: misc_feature

206 <222> LOCATION: 205

207 <223> OTHER INFORMATION: n = a, g, c, or t/u

W--> 209 <400> 3

210 atg ggt gca ggt gga aga atg caa gtg tct cct ccc tcc aag aag tct 48
 211 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
 212 1 5 10 15
 214 gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act 96
 215 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
 216 20 25 30
 218 gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg 144
 219 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 220 35 40 45
 222 atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc 192
 223 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
 224 50 55 60

W--> 226 tgc ttc tac tac ntc gcc acc act tac ttc cct ctc ctc cct cac cct 240

227 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
 228 65 70 75 80
 230 ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc 288
 231 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 232 85 90 95
 234 cta acc ggc gtc tgg gtc ata gcc cac aag tgc ggc cac cac gcc ttc 336
 235 Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe
 236 100 105 110
 238 agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc 384
 239 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 240 115 120 125
 242 ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cgc agc cac 432
 243 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
 244 130 135 140

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TIME: 12:18:15

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Output Set: N:\CRF4\02242003\I771904A.raw

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246 cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag      480
247 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
248 145                               150                               155                               160
250 aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg      528
251 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
252                               165                               170                               175
254 gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg ccg ttg      576
255 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
256                               180                               185                               190
258 tac tta gcc ttc aac gtc tcg gga aga cct tac gac ggc ggc ttc cgt      624
259 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
260                               195                               200                               205
262 tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc      672
263 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
264                               210                               215                               220
266 cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc      720
267 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
268 225                               230                               235                               240
272 ttc cgt tac gcc gcc ggc cag gga gtg gcc tcg atg gtc tgc ttc tac      768
273 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
274                               245                               250                               255
276 gga gtc ccg ctt ctg att gtc aat ggt ttc ctc gtg ttg atc act tac      816
277 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
278                               260                               265                               270
280 ttg cag cac acg cat cct tcc ctg cct cac tac gat tcg tcc gag tgg      864
281 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
282                               275                               280                               285
284 gat tgg ttc agg gga gct ttg gct acc gtt gac aga gac tac gga atc      912
285 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
286                               290                               295                               300
288 ttg aac aag gtc ttc cac aat att acc gac acg cac gtg gcc cat cat      960
289 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
290 305                               310                               315                               320
292 ccg ttc tcc acg atg ccg cat tat cac gcg atg gaa gct acc aag gcg      1008
293 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
294                               325                               330                               335
296 ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg      1056
297 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
298                               340                               345                               350
300 gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg      1104
301 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
302                               355                               360                               365
304 gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta      1152
305 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
306                               370                               375                               380
308 tga                                                                    1155
310 <210> SEQ ID NO: 4
311 <211> LENGTH: 384
312 <212> TYPE: PRT

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/771,904A

DATE: 02/24/2003
TIME: 12:18:16

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\02242003\I771904A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 205 ✓

Seq#:1; Xaa Pos. 69 ✓

Seq#:2; Xaa Pos. 69 ✓

Seq#:3; N Pos. 205 ✓

Seq#:3; Xaa Pos. 69

Seq#:4; Xaa Pos. 69